Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:08:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231719.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6231719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:08:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,272,180
Mapped reads	219,194 / 17.23%
Unmapped reads	1,052,986 / 82.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,020 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	21,063 / 1.66%
Duplication rate	7.48%
Clipped reads	142,236 / 11.18%

2.2. ACGT Content

Number/percentage of A's	3,515,068 / 26.76%
Number/percentage of C's	2,595,754 / 19.76%
Number/percentage of T's	3,999,685 / 30.45%
Number/percentage of G's	3,023,534 / 23.02%
Number/percentage of N's	2,263 / 0.02%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0042

Standard Deviation	0.1055

2.4. Mapping Quality

Mean Mapping Quality	38.35

2.5. Mismatches and indels

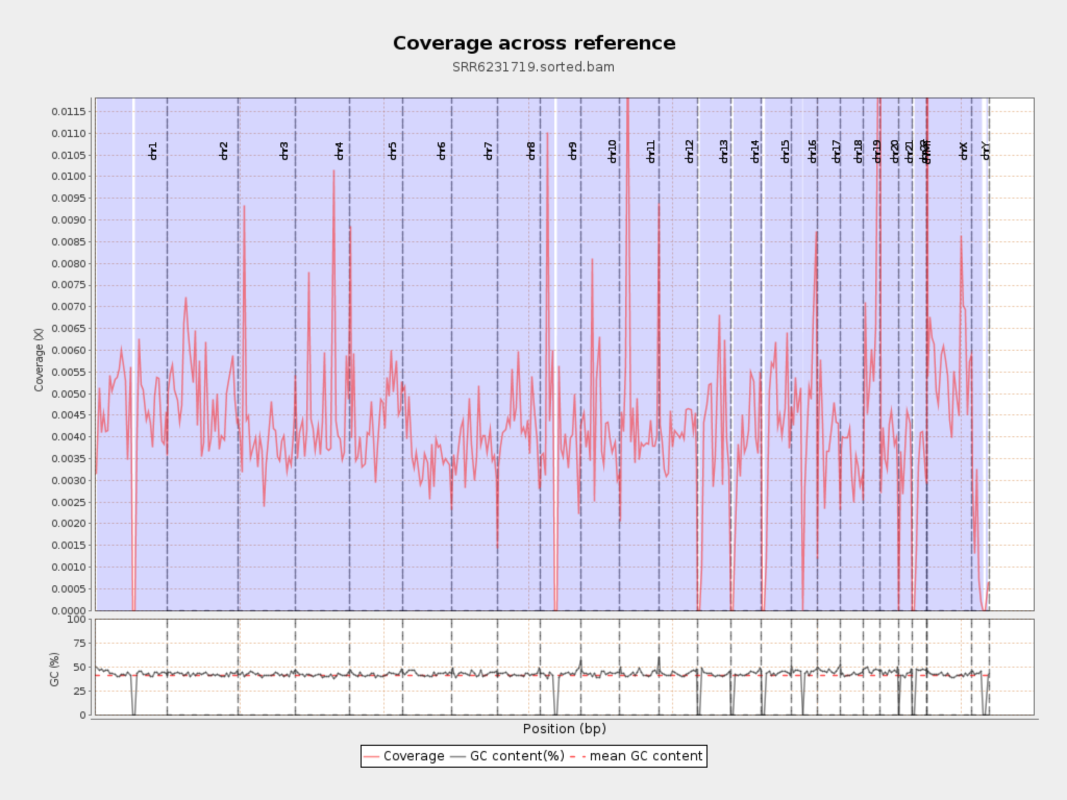
General error rate	0.99%
Mismatches	123,776
Insertions	2,296
Mapped reads with at least one insertion	1.02%
Deletions	3,889
Mapped reads with at least one deletion	1.74%
Homopolymer indels	36.2%

2.6. Chromosome stats

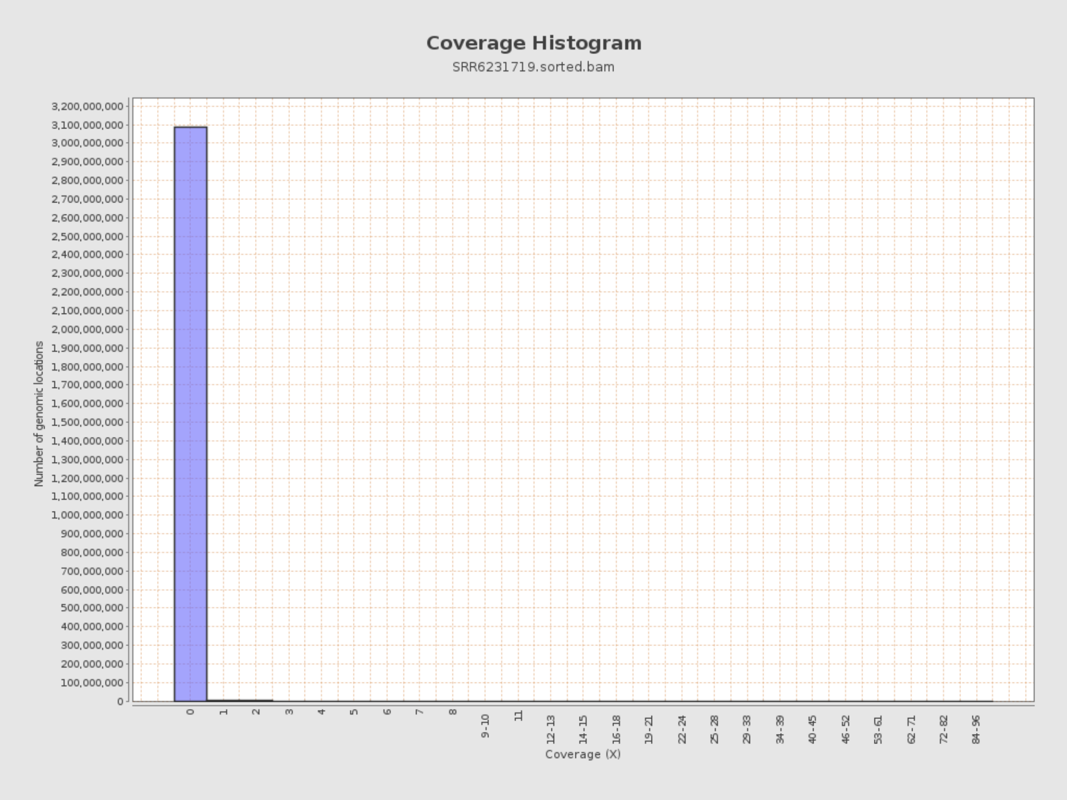
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1116491	0.0045	0.1176
chr2	243199373	1225508	0.005	0.1174
chr3	198022430	790868	0.004	0.0953
chr4	191154276	876574	0.0046	0.1053
chr5	180915260	802730	0.0044	0.1032
chr6	171115067	616913	0.0036	0.0922
chr7	159138663	602862	0.0038	0.0969

chr8	146364022	632205	0.0043	0.1034
chr9	141213431	556028	0.0039	0.0923
chr10	135534747	573840	0.0042	0.1026
chr11	135006516	626768	0.0046	0.1091
chr12	133851895	539886	0.004	0.0969
chr13	115169878	431881	0.0037	0.1388
chr14	107349540	380284	0.0035	0.1084
chr15	102531392	408989	0.004	0.0924
chr16	90354753	423423	0.0047	0.1198
chr17	81195210	330355	0.0041	0.1062
chr18	78077248	272038	0.0035	0.0968
chr19	59128983	447478	0.0076	0.1316
chr20	63025520	239132	0.0038	0.0952
chr21	48129895	162305	0.0034	0.0866
chr22	51304566	129760	0.0025	0.0715
chrMT	16571	11153	0.673	1.334
chrX	155270560	883578	0.0057	0.1171
chrY	59373566	62229	0.001	0.0478

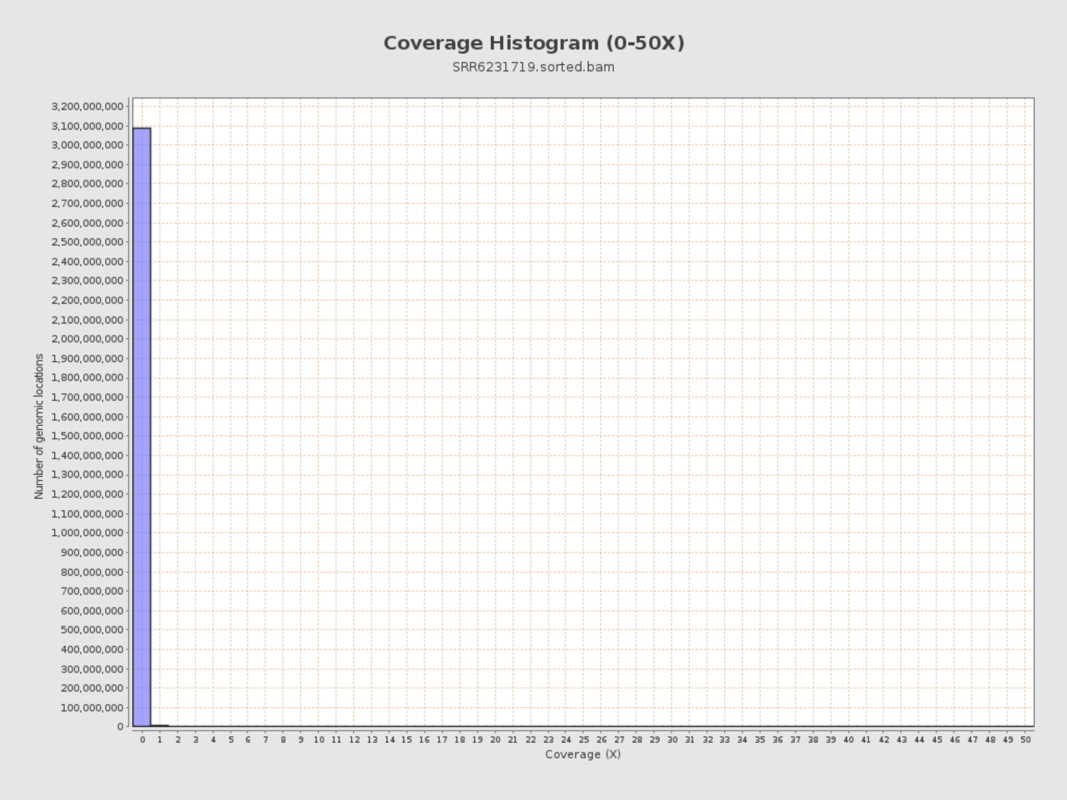
3. Results : Coverage across reference



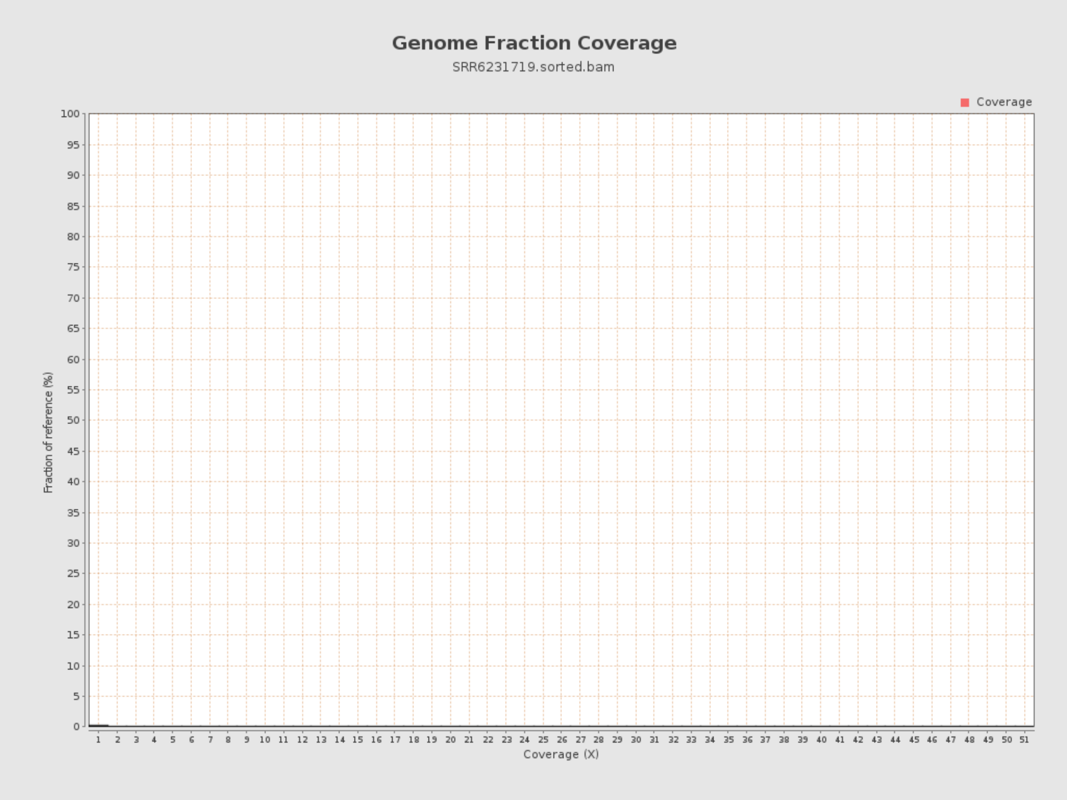
4. Results : Coverage Histogram



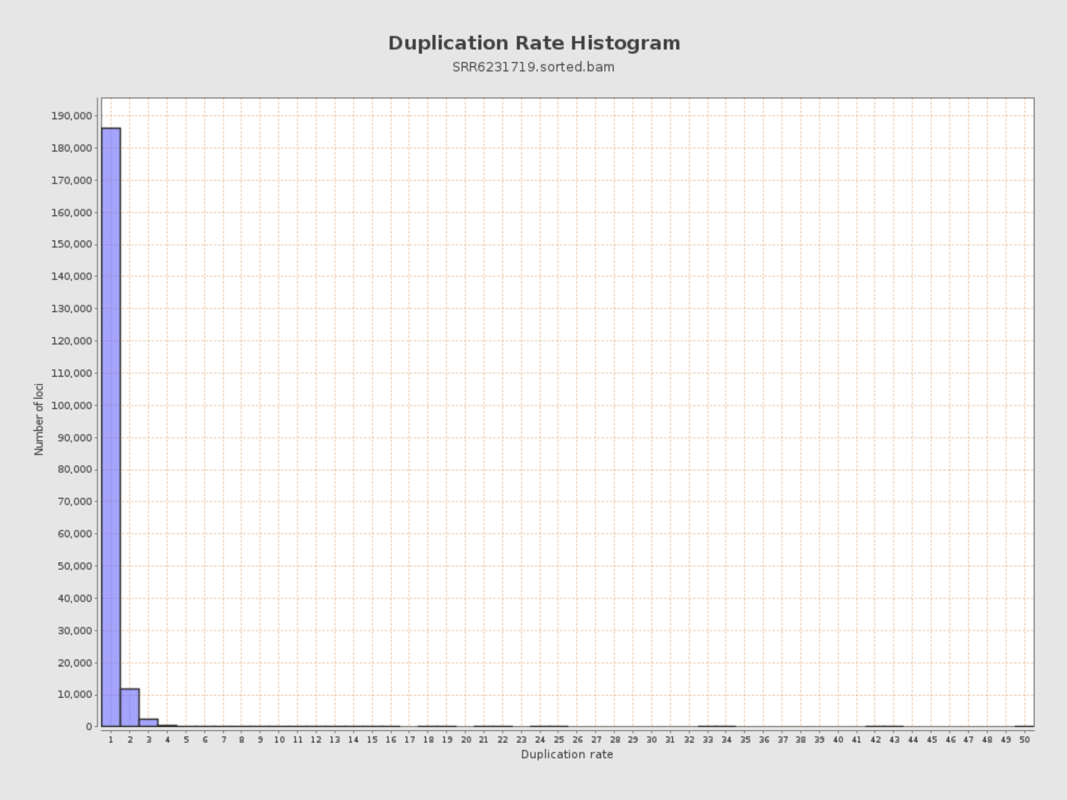
5. Results : Coverage Histogram (0-50X)



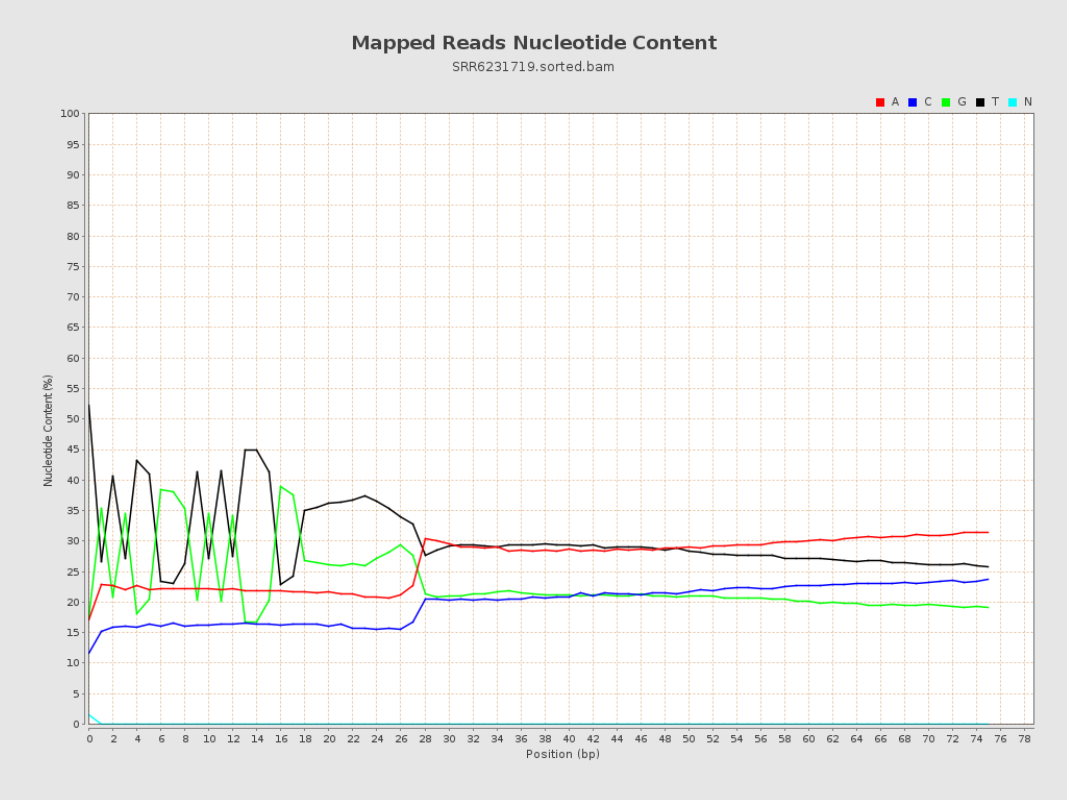
6. Results : Genome Fraction Coverage



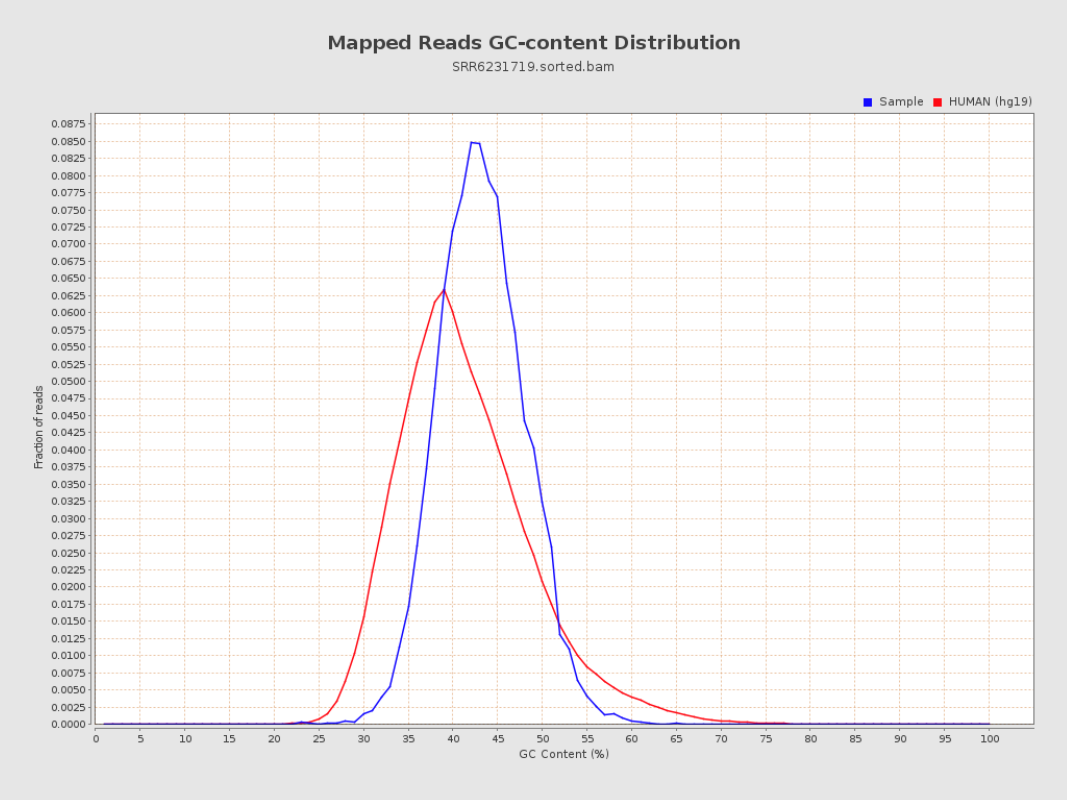
7. Results : Duplication Rate Histogram



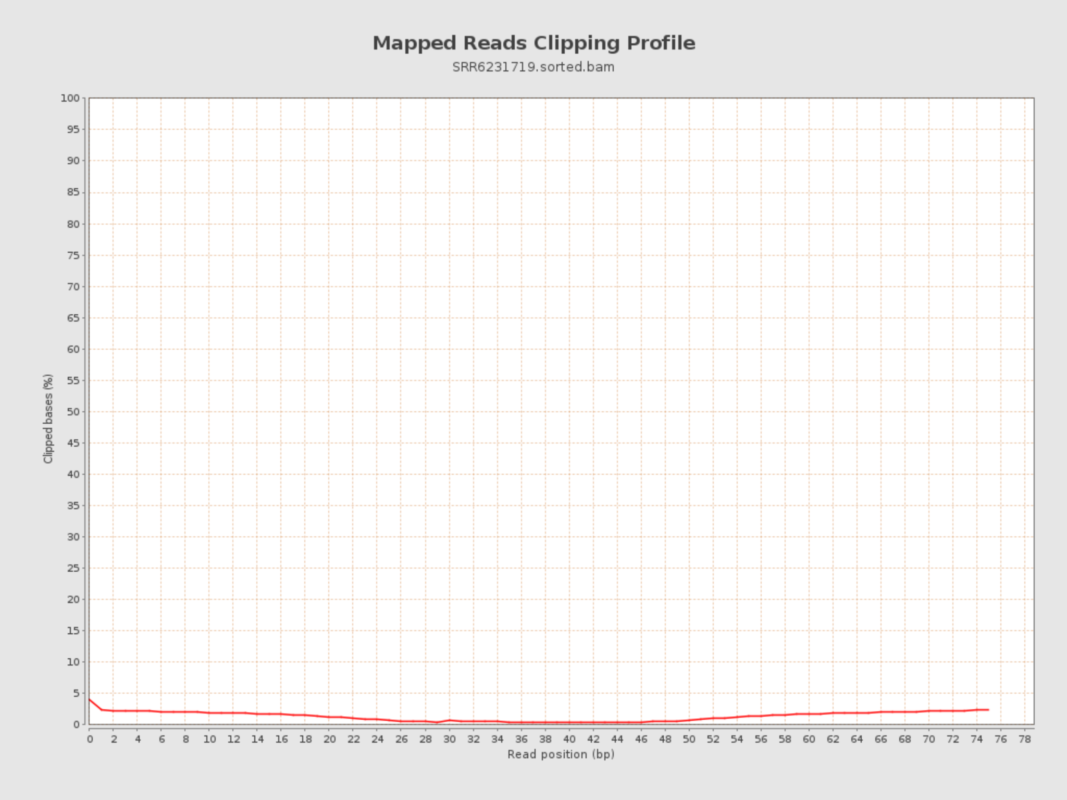
8. Results : Mapped Reads Nucleotide Content



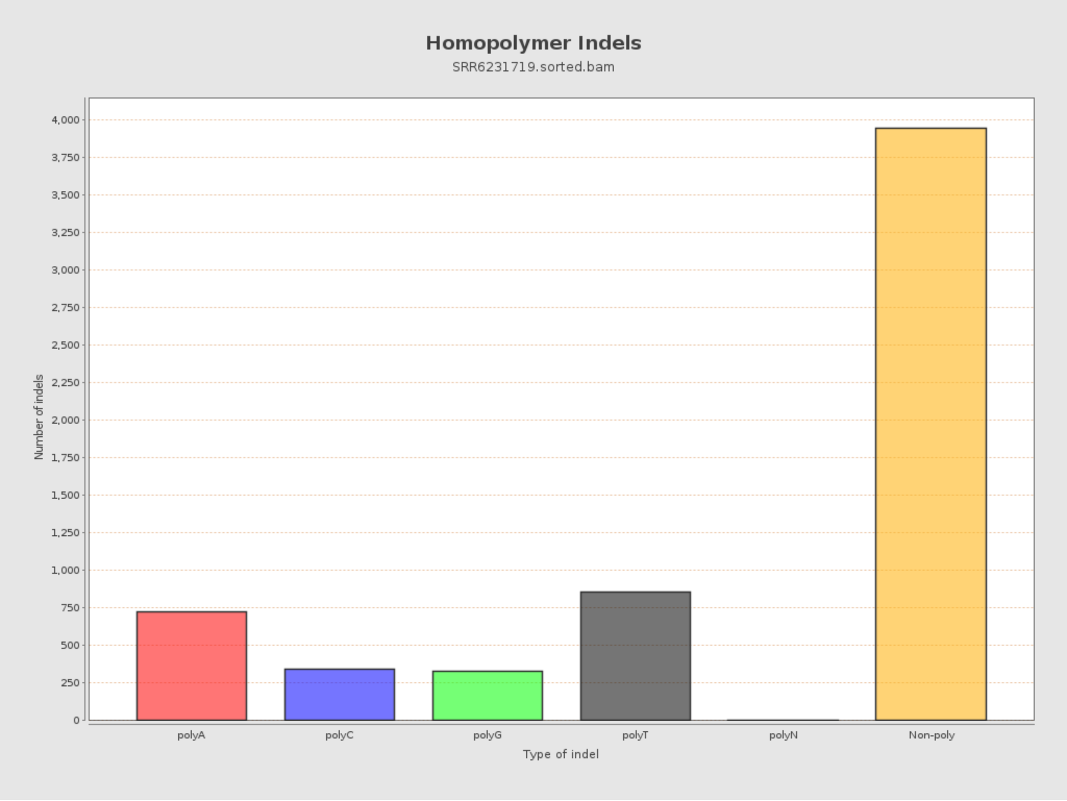
9. Results : Mapped Reads GC-content Distribution



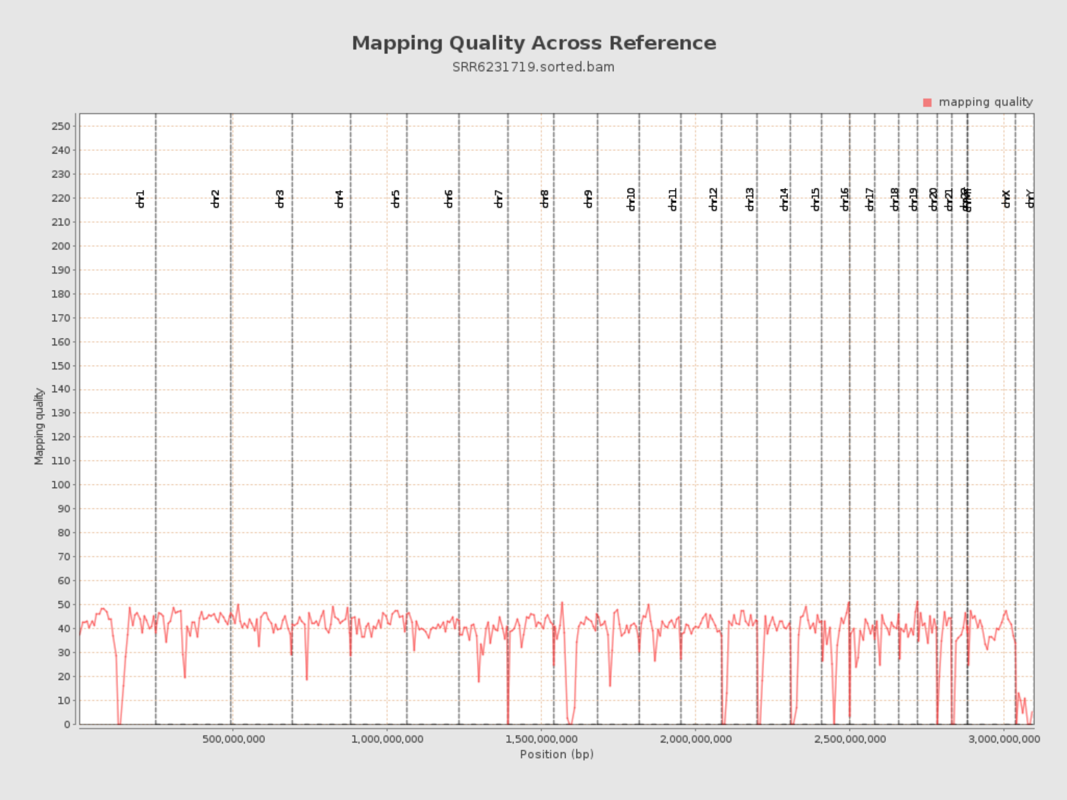
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram